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<110> Novozymes A/S

Jorgensen, Steen T

Rasmussen, Michael D

Andersen, Jens Tonne

Olsen, Carsten

<120> Multiple Insertion of Genes

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<140> 09/928847

<141> 2001-08-13

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<170> PatentIn version 3.1

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                                             1

cca ttc tat aga aag aca tgg gcc gaa atc gat tta acg gct tta aaa      1362
Pro Phe Tyr Arg Lys Thr Trp Ala Glu Ile Asp Leu Thr Ala Leu Lys
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Met Ala Val Val Lys Ala Asn Ala Tyr Gly His Gly Asp Ala Gln Val
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gcg aag gcg gct ctt gca gaa ggg gcg tcc att ctt gct gtg gct tta      1506
Ala Lys Ala Ala Leu Ala Glu Gly Ala Ser Ile Leu Ala Val Ala Leu
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ttg gat gaa gcg ctt tcg ctg agg gcg cag ggg att gaa gaa ccg att      1554
Leu Asp Glu Ala Leu Ser Leu Arg Ala Gln Gly Ile Glu Glu Pro Ile
        70              75              80

ctt gtc ctc ggt gca gtg ccg acc gaa tat gca agc att gcc gcg gaa      1602
Leu Val Leu Gly Ala Val Pro Thr Glu Tyr Ala Ser Ile Ala Ala Glu
85              90              95              100

aag cgc att atc gtg act ggc tac tcc gtc ggc tgg ctg aaa gac gtg      1650
Lys Arg Ile Ile Val Thr Gly Tyr Ser Val Gly Trp Leu Lys Asp Val
            105             110             115

ctc ggt ttt ctg aat gag gcc gaa gct cct ctt gaa tat cat ttg aag      1698
Leu Gly Phe Leu Asn Glu Ala Glu Ala Pro Leu Glu Tyr His Leu Lys
            120             125             130

atc gac acg ggc atg ggc cgc ctt ggc tgc aaa acg gaa gaa gag atc      1746
Ile Asp Thr Gly Met Gly Arg Leu Gly Cys Lys Thr Glu Glu Glu Ile
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aaa gaa atg atg gag atg acc gaa tcg aac gat aag ctc aat tgt acg      1794
Lys Glu Met Met Glu Met Thr Glu Ser Asn Asp Lys Leu Asn Cys Thr
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ggc gtg ttc act cat ttc gcc acg gcg gac gaa aag gac acc gat tat      1842
Gly Val Phe Thr His Phe Ala Thr Ala Asp Glu Lys Asp Thr Asp Tyr
165             170             175             180

ttc aac atg cat ctt gac cgc ttt aaa gag ctg atc agc ccc ttc ccg      1890
Phe Asn Met His Leu Asp Arg Phe Lys Glu Leu Ile Ser Pro Phe Pro
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ctt gac cgt ttg atg gtg cat tcg tca aac agc gcc gcg ggt ctg cgc      1938
Leu Asp Arg Leu Met Val His Ser Ser Asn Ser Ala Ala Gly Leu Arg
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Phe Arg Glu Gln Leu Phe Asn Ala Val Arg Phe Gly Ile Gly Met Tyr
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cgg gaa gtg ttt tcg ctt cat acc gaa ctc acc cat gtg aaa aaa att      2082
Arg Glu Val Phe Ser Leu His Thr Glu Leu Thr His Val Lys Lys Ile
245             250             255             260

aaa aaa ggc gag agc gtc agc tac ggg gcg aca tat aca gct cag cgc      2130
Lys Lys Gly Glu Ser Val Ser Tyr Gly Ala Thr Tyr Thr Ala Gln Arg
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Arg Arg Leu Ala Gly Thr Glu Val Leu Ile Asp Gly Lys Arg Gln Lys
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ata gca ggg aga atc tgc atg gac cag ttc atg att tcc ctt gcc gaa      2274
Ile Ala Gly Arg Ile Cys Met Asp Gln Phe Met Ile Ser Leu Ala Glu
        310                 315                 320

gaa tac cct gtc ggc aca aag gtt acc ttg atc gga aag caa aaa gac      2322
Glu Tyr Pro Val Gly Thr Lys Val Thr Leu Ile Gly Lys Gln Lys Asp
325                 330                 335                 340

gaa tgg atc tca gtc gac gaa atc gcc caa aat ttg cag acg atc aat      2370
Glu Trp Ile Ser Val Asp Glu Ile Ala Gln Asn Leu Gln Thr Ile Asn
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tat gaa att acc tgt atg ata agt tca agg gtg ccc cgt atg ttt ttg      2418
Tyr Glu Ile Thr Cys Met Ile Ser Ser Arg Val Pro Arg Met Phe Leu
                360                 365                 370

gaa aat ggg agt ata atg gaa ata agg aat ccg atc ttg cct gat caa      2466
Glu Asn Gly Ser Ile Met Glu Ile Arg Asn Pro Ile Leu Pro Asp Gln
        375                 380                 385

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His Val Arg Leu Met Ala Val Val Lys Ala Asn Ala Tyr Gly His Gly
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Ala Val Ala Leu Leu Asp Glu Ala Leu Ser Leu Arg Ala Gln Gly Ile
65   70   75   80

Glu Glu Pro Ile Leu Val Leu Gly Ala Val Pro Thr Glu Tyr Ala Ser
                85   90   95

Ile Ala Ala Glu Lys Arg Ile Ile Val Thr Gly Tyr Ser Val Gly Trp
            100   105   110

Leu Lys Asp Val Leu Gly Phe Leu Asn Glu Ala Glu Ala Pro Leu Glu
        115   120   125

Tyr His Leu Lys Ile Asp Thr Gly Met Gly Arg Leu Gly Cys Lys Thr
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Glu Glu Glu Ile Lys Glu Met Met Glu Met Thr Glu Ser Asn Asp Lys
145   150   155   160

Leu Asn Cys Thr Gly Val Phe Thr His Phe Ala Thr Ala Asp Glu Lys
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Asp Thr Asp Tyr Phe Asn Met His Leu Asp Arg Phe Lys Glu Leu Ile
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Ser Pro Phe Pro Leu Asp Arg Leu Met Val His Ser Ser Asn Ser Ala
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Ala Gly Leu Arg Phe Arg Glu Gln Leu Phe Asn Ala Val Arg Phe Gly
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Val Lys Lys Ile Lys Lys Gly Glu Ser Val Ser Tyr Gly Ala Thr Tyr
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Thr Ala Gln Arg Asp Glu Trp Ile Gly Thr Val Pro Val Gly Tyr Ala
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Asp Gly Trp Leu Arg Arg Leu Ala Gly Thr Glu Val Leu Ile Asp Gly
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Lys Arg Gln Lys Ile Ala Gly Arg Ile Cys Met Asp Gln Phe Met Ile
305             310             315             320

Ser Leu Ala Glu Glu Tyr Pro Val Gly Thr Lys Val Thr Leu Ile Gly
            325             330             335

Lys Gln Lys Asp Glu Trp Ile Ser Val Asp Glu Ile Ala Gln Asn Leu
            340             345             350

Gln Thr Ile Asn Tyr Glu Ile Thr Cys Met Ile Ser Ser Arg Val Pro
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cagccgaatc aatcgttttc tccaattcct cttttgactc gggaactccg tttttcgaga    3780

tttcttcctt gactttggcc atcagcgctg acgcgttttc actgccgatt ttctcgccaa    3840

gctctgaagt ggtgacaagc tcttcattcg cgaccttttt cacatcttcg gaaattttt    3900

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<211> 6837

<212> DNA

<213> Artificial Sequence

<220>

<223> Plasmid pMOL 1642

<220>

<221> misc_feature

<222> (669)..(669)

<223> n denotes an undetermined nucleotide


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aattgttaat catgttggag ctcagtgaga gcgaagcgaa cacttgattt tttaattttc     240

tatcttttat aggtcattag agtatactta tttgtcctat aaactattta gcagcataat     300

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atttgaagaa cccgaggatc catgctgtcc agactgtccg ctgtgtaaaa aataggaata     420

aaggggggtt gttattattt tactgatatg taaaatataa tttgtataag aaaatgagag     480

ggagaggaaa catgaagaag attgcaattg cggcgattac agcgacaagc gtgctggctc     540

tcagcgcatg cagcggggga gattctgagg ttgttgcgga aacaaaagct ggaaatatta     600
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- 27-

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ataacataaa agtaaccgat gatgacgtaa aagaatatta tgacggcctg aaaggcaaaa    900

tccacttaag ccacattctt gtgaaagaaa agaaaacggc tgaagaagtt gagaaaaagc    960

tgaaaaaagg cgaaaaattc gaagaccttg caaaagagta ttcggtaccc gggtctagag   1020

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caattcctgc atgttttaag gaattgttaa attgatttt tgtaaatatt ttcttgtatt   1260

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- 28-

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caaagaggtt acagaacgag aacataaagc gatggatcag tacaagaaag atactgtatt   2880

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<220>

<223> Primer

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taagcttgaa ttcggaggcc gttattatat catgagcgaa aatgtaataa aagaaactga     240

aaacaagaaa aattcaagag gacgtaattg gacatttgtt ttatatccag aatcagcaaa     300

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tgaattatta agaaaacaa caacagatag atataaatta attaaagaaa tgattgagtt      660

tattgatgaa caaggaatcg tagaatttaa gagtttaatg gattatgcaa tgaagtttaa     720

atttgatgat tggttcccgc ttttatgtga taactcggcg tatgttattc aagaatatat     780

aaaatcaaat cggtataaat ctgaccgata gggatcc                               817
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- 31-